

5' AGC TCG AGG GAC GGC ACC ATG GAG GAC TCC GAG GCG GTG CAG AGG GCC ACA CGC

	10	19	28	37	46	55
CTC ATC	GAG CAG CGG CTG GCA CAG GAG GAG AAT GAG AAA CTC CGA GGA GAC					
L I	E Q R L A Q E E N E K L R G D					
ACA CGC	CAG AAG CTG CCC ATG GAC TTTG CTG GAG GAT GAG AAG CAC CAC	64	73	82	91	109
T R	Q K L P M D L V L E D E K H H	118	127	136	145	163
GGG GCT	GCT AGT GCA GCC CTG CAG AAG GTG AAG GGC CAA GAG CGC GTG CGC AAG	172	181	190	199	217
G A	Q S A A L Q K V K G Q E R V R K	226	235	244	253	262
ACG TCC	CTG GAC CTG CGG CGG GAG ATC ATC GAT GTG GGC GGG ATC CAG AAC CTC					271
T S	L D L R R E I I D V G G I Q N L					
ATC GAG	CTG CGG AAG AAA CGC AAG CAG AAG AAG CGG GAC GCT CTG GCC GCC TCG	280	289	298	307	316
I E	L R K K R K Q K R D A L A A S					325

FIGURE 1A

T C G T T G E G S G S C G

CAT	GAG	CCG	CCC	CCA	GAG	CCC	GAG	GAG	ATC	ACT	GGC	CCT	GTG	GAT	GAG	GAG	ACC	379
H	E	P	P	P	E	P	E	E	I	T	G	P	V	D	E	E	T	
TTC	CTG	AAA	GCT	GCG	GTG	GAG	GGG	AAA	ATG	AAG	GTC	ATT	GAG	AAG	TTC	CTG	GCT	433
F	L	K	A	A	V	E	G	K	M	K	V	I	E	K	F	L	A	
GAC	GGG	GGG	TCA	GCC	GAC	ACG	TGC	GAC	CAG	TTC	CGT	CGG	ACA	GCA	CTG	CAC	CGA	487
D	G	G	S	A	D	T	C	D	Q	F	R	R	T	A	L	H	R	
GCT	TCC	CTG	GAA	GGC	CAC	ATG	GAA	ATC	CTG	GAG	AAG	CTT	CTA	GAT	AAT	GGG	GCC	541
A	S	L	E	G	H	M	E	I	L	E	K	L	L	D	N	G	A	
ACT	GTG	GAC	TTC	CAG	GAT	CGG	CTG	GAC	TGC	ACA	GCC	ATG	CAT	TGG	GCC	TGC	CGC	595
T	V	D	F	Q	D	R	L	D	C	T	A	M	H	W	A	C	R	
GGG	GGC	CAC	TTA	GAG	GTG	GTG	AAA	CTT	CTG	CAA	AGC	CAT	GGA	GCA	GAC	ACC	AAT	649
G	G	H	L	E	V	V	K	L	L	Q	S	H	G	A	D	T	N	

FIGURE 1B

T G G T T G E G G G G G

GTG	AGG	GAT	AAG	CTG	CTG	AGC	ACC	CCG	CTG	CAC	GTC	GCA	GTC	CGG	ACA	GGG	CAG	703
V	R	D	K	L	L	S	T	P	L	H	V	A	V	R	T	G	Q	
GTG	GAG	ATT	GTG	GAG	CAC	TTT	CTA	TCC	CTG	GGC	CTG	GAA	ATC	AAT	GCC	AGA	GAC	757
V	E	I	V	E	H	F	L	S	L	G	L	E	I	N	A	R	D	
AGG	GAA	GGG	GAT	ACT	GCC	CTG	CAT	GAC	GCT	GTG	AGG	CTC	AAC	CGC	TAC	AAA	ATC	811
R	E	G	D	T	A	L	H	D	A	V	R	L	N	R	Y	K	I	
ATC	AAA	CTG	CTG	CTG	CTG	CAT	GGG	GCT	GAC	ATG	ATG	ACC	AAG	AAC	CTG	GCA	GGA	865
I	K	L	L	L	L	H	G	A	D	M	M	T	K	N	L	A	G	
AAG	ACC	CCG	ACG	GAC	CTG	GTG	CAG	CTC	TGG	CAG	GCT	GAT	ACC	CGG	CAC	GCC	CTG	919
K	T	P	T	D	L	V	Q	L	W	Q	A	D	T	R	H	A	L	
GAG	CAT	CCT	GAG	CCG	GGG	GCT	GAG	CAT	AAC	GGG	CTG	GAG	GGG	CCT	AAT	GAT	AGT	973
E	H	P	E	P	G	A	E	H	N	G	L	E	G	P	N	D	S	
658					667				676			685		694				

FIGURE 1C

TTT TCT TCC TCA TGA TGC TGT TAT TAC

GGG	CGA	GAG	ACC	CCT	CAG	CCT	GTG	CCA	GCC	CAG	TGA	ATG	CGT	GCC	CCA	GCC	CAG
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
G	R	E	T	P	Q	P	V	P	A	A	Q	-	-	-	-	-	-
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1036	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
CCA	GCT	ACC	CAG	CCC	CTC	TCT	GTG	TGC	AGC	CGG	AGG	GTC	CTA	AGA	ATG	GCT	CCC
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1090	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
GGA	GCT	AAC	TGA	GGG	CCC	AGC	CTT	TTT	TCT	GCA	TGA	TCC	AGG	AGC	ACA	TAC	CAC
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1144	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
AAA	CTA	CCA	CAA	TAA	AAA	AGC	TG	3'	-	-	-	-	-	-	-	-	-
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

FIGURE 1D

1	S M E D S E A V Q R A T A L I E Q R L A - M E G P E A V Q R A T E L I E Q R L A - M E G P E A V Q R A T E L I E Q R L A	5578191CD1 99501360 95420272
21	Q E E E N E K L R G D T R Q K L P M D L Q E E E T E K L R R S A P G K L S M D M Q E E E T E K L R R S A P G K L S M D M	5578191CD1 99501360 95420272
20	L V L E D E K H H G A Q S A A L Q K V K L V L E E E K R L G V Q S P A L Q K V K L V L E E E K R L G V Q S P A L Q K V K	5578191CD1 99501360 95420272
41	G Q E R V R K T S L D L R R E I I D V G G Q E R V R K T S L D L R R E I I D V G G Q E R V R K T S L D L R R E I I D V G	5578191CD1 99501360 95420272
61	G I Q N L I E L R K K R K Q K R D A L G I Q N L I E L R K K R K Q K R D A L G I Q N L I E L R K K R K Q K R D A L	5578191CD1 99501360 95420272
81		
80		
80		

FIGURE 2A

101	A A S H E P P P E P E I T G P V D E E	5578191CD1
100	A A A Q E P P P E P E I T G P V N E E	g9501360
100	A A A Q E P P P E P E I T G P V N E E	g5420272
121	T F L K A A V E G K M K V I E K F L A D	5578191CD1
120	T F L K A A V E G K M K V I D K Y L A D	g9501360
120	T F L K A A V E G K M K V I D K Y L A D	g5420272
141	G G S A D T C D Q F R R T A L H R A S L	5578191CD1
140	G G S A D T C D E F R R T A L H R A S L	g9501360
140	G G S A D T C D E F R R T A L H R A S L	g5420272
161	E G H M E I L E K L L D N G A T V D F Q	5578191CD1
160	E G H M E I L E K L L E N G A T V D F Q	g9501360
160	E G H M E I L E K L L E N G A T V D F Q	g5420272
181	D R L D C T A M H W A C R G G H L E V V	5578191CD1
180	D R L D C T A M H W A C R G G H L E V V	g9501360
180	D R L D C T A M H W A C R G G H L E V V	g5420272

FIGURE 2B

201	K L L Q S H G A D T N V R D K L L S T P	5578191CD1
200	R L L Q S R G A D T N V R D K L L S T P	99501360
200	R L L Q S R G A D T N V R D K L L S T P	95420272
221	L H V A V R T G Q V E I V E H F L S L G	5578191CD1
220	L H V A V R T G H V E I V E H F L S L G	99501360
220	L H V A V R T G H V E I V E H F L S L G	95420272
241	L E I N A R D R E G D T A L H D A V R L	5578191CD1
240	L D I N A K D R E G D S A L H D A V R L	99501360
240	L D I N A K D R E G D S A L H D A V R L	95420272
261	N R Y K I I K L L L H G A D M M T K N	5578191CD1
260	N R Y K I I K L L L H G A D M M A K N	99501360
260	N R Y K I I K L L L H G A D M M A K N	95420272
281	L A G K T P T D L V Q L W Q A D T R H A	5578191CD1
280	L A G K T P T D L V Q L W Q A D T R H A	99501360
280	L A G K T P T D L V Q L W Q A D T R H A	95420272

FIGURE 2C

FIGURE 2D

301	L E H P E P G A E H N G L E G P N D S G	5578191CD1
300	L E H P E P E S E Q N G L E R P - G S G	g9501360
300	L E H P E P E S E Q N G L E R P - G S G	g5420272
321	R E T P Q P V P A Q	5578191CD1
319	R E T P Q P I P A Q	g9501360
319	R E T P Q P I P A Q	g5420272

Tissue Distribution

Tissue Category	Clone Count	Found in	Abs Abund	Pct Abund
Cardiovascular System	266190	4/68	4	0.0015
Connective Tissue	144645	0/47	0	0.0000
Digestive System	501101	1/148	1	0.0002
Embryonic Structures	106713	0/21	0	0.0000
Endocrine System	225386	2/53	2	0.0009
Exocrine Glands	254635	0/64	0	0.0000
Genitalia, Female	427284	0/106	0	0.0000
Genitalia, Male	448207	3/114	7	0.0016
Germ Cells	38282	0/5	0	0.0000
Hemic and Immune System	680277	0/159	0	0.0000
Liver	109378	0/35	0	0.0000
Musculoskeletal System	159280	10/47	24	0.0151
Nervous System	955753	4/198	5	0.0005
Pancreas	110207	0/24	0	0.0000
Respiratory System	390086	1/93	2	0.0005
Sense Organs	19256	0/8	0	0.0000
Skin	72292	0/15	0	0.0000
Stomatognathic System	12923	0/10	0	0.0000
Unclassified/Mixed	120926	1/13	1	0.0008
Urinary Tract	279062	3/64	5	0.0018
Totals	5321883	29/1292	51	0.0000

FIGURE 3A

Found in:

Library ID	Clone Count	Library Description	Abs Abund	Pct Abund
MUSCNOT10	3302	muscle, gluteal, mw/clear cell SAR, 43F	11	0.3331
MUSLTDT01	804	muscle, thigh, mw/liposAR, 58M	1	0.1244
MUSCNOT02	2541	muscle, psoas, 12M	3	0.1181
MUSLNOT01	3306	muscle, tibial, aw/thrombosis, 41F	2	0.0605
MUSLTDR02	4002	muscle, thigh, mw/liposAR, 58M, RP	2	0.0500
MUSCNOM01	2716	muscle, skeletal, mw/malignant hyperthermia	1	0.0368
MUSCDIN06	3043	muscle, thigh, ALS, 74F, NORM	1	0.0329
MUSCDMT01	3137	muscle, calf, mw/gangrene, aw/atherosclerosis	1	0.0319
MUSCDIT06	3192	muscle, skeletal, aw/Krabbe, 11mF	1	0.0313
MUSCNOR07	6491	muscle, forearm, mw/intramuscular hemangioma	1	0.0154

FIGURE 3B

FIGURE 4A

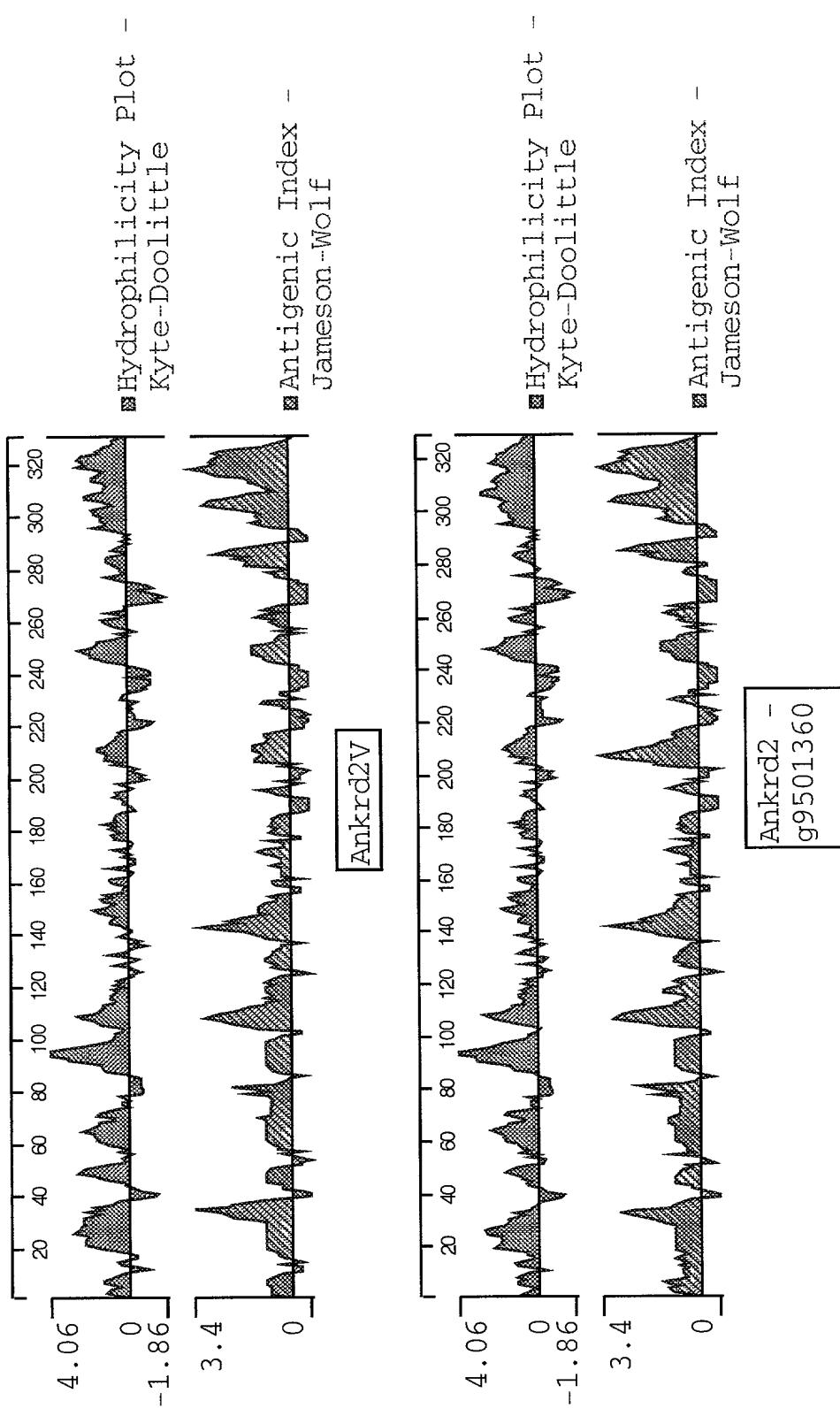


FIGURE 4B

